

IN THE CLAIMS:

All claims currently pending and under consideration in the referenced application are shown in the listing of claims and will replace all prior versions and listings of claims in the application. Claims 18-23 were previously cancelled. Claims 1-4, 6-9, 36 and 39 are amended herein. Claims 5, 10-17, 24-35, 37 and 38 are cancelled herein. All amendments and cancellations have been made without prejudice or disclaimer. Claims 41-45 are added herein. No new matter has been added. Please enter these claims as amended.

Listing of the Claims:

1. (Currently amended) A method for selecting an animal ~~for having desired genotypic properties comprising testing said animal for the presence of~~ a parentally imprinted quantitative trait locus (QTL) associated with muscle mass and/or fat deposition in the animal, the method comprising:

testing the animal for the presence of the parentally imprinted QTL associated with muscle mass and/or fat deposition in the animal.

2. (Currently amended) The method according to claim 1, further comprising testing a nucleic acid sample from said animal for the presence of ~~[[a]]~~ the parentally imprinted QTL.

3. (Currently amended) The method according to claim 1, wherein said animal is a pig and in said pig said parentally imprinted QTL is located at chromosome 2.

4. (Currently amended) The method according to claim 1, wherein said animal is a pig and in said pig said parentally imprinted QTL maps at about position 2p1.7.

5. (Cancelled).

6. (Currently amended) The method according to ~~claim 5~~ claim 1 wherein said parentally imprinted QTL comprises at least a part of an insulin-like growth factor-2 gene (IGF-

2).

7. (Currently amended) The method according to claim 1, wherein said animal is a pig and in said pig said parentally imprinted QTL comprises a genetic marker characterized as nt241(G-A) or as Swc9.

8. (Currently amended) The method according to claim 1 wherein a paternal allele of said parentally imprinted QTL is predominantly expressed in said animal.

9. (Currently amended) The method according to claim 1 wherein a maternal allele of said parentally imprinted QTL is predominantly expressed in said animal.

10-35. (Cancelled)

36. (Currently amended) The method according to claim 1 wherein said testing comprises utilizing an isolated and/or recombinant nucleic acid comprising [[a]] the parentally imprinted QTL or a functional fragment of said parentally imprinted QTL comprising genetic information capable of influencing a quantitative trait of said animal.

37-38. (Cancelled)

39. (Currently amended) A method of selecting an animal having a desired muscle mass and/or fat deposition trait, said method comprising:

associating ~~a phenotype~~ the desired muscle mass and/or fat deposition trait with a parentally imprinted quantitative trait locus;

mapping the parentally imprinted quantitative trait locus to a locus in a genome in the species of the animal;

obtaining a nucleic acid sample from the animal; and

determining whether the parentally imprinted quantitative trait locus is present in the nucleic acid sample from the animal;

wherein the parentally imprinted quantitative trait locus is present in the nucleic acid sample,

thus selecting the animal having the desired muscle mass and/or fat deposition trait.

40. (Previously presented) The method according to claim 39, further comprising:

linking a genetic marker to the parentally imprinted quantitative trait locus;

wherein determining whether the parentally imprinted quantitative trait locus is present in the nucleic acid sample from the animal comprises testing the nucleic acid sample for the genetic marker's presence.

41. (New) A method for selecting a pig having a paternally imprinted quantitative trait locus (QTL) on chromosome 2 of the pig associated with a desired muscle mass and/or fat deposition in the pig, said method comprising:

identifying the presence of the paternally imprinted QTL on chromosome 2 of the pig by detecting one or more genetic markers selected from the group consisting of genetic markers linked to the paternally imprinted QTL on chromosome 2 of the pig, genetic markers in linkage disequilibrium with the paternally imprinted QTL on chromosome 2 of the pig, genetic markers that represent the actual causal mutation or mutations affecting muscle mass and/or fat deposition in the pig within the paternally imprinted QTL on chromosome 2 of the pig, and combinations of any thereof,

wherein the location of the paternally imprinted QTL on chromosome 2 of the pig is indicated by a genomic region comprising the genetic markers Swr2516, Swc9, S22623 and Swr783 on chromosome 2 of the pig, and

wherein the parentally imprinted QTL is present on chromosome 2 of the pig,
thus selecting the pig.

42. (New) The method according to claim 41, further comprising testing a nucleic acid sample from the pig for the presence of the paternally imprinted QTL on chromosome 2 of the pig.

43. (New) The method according to claim 41, wherein the paternally imprinted QTL on chromosome 2 of the pig maps at about position 2p1.7.

44. (New) The method according to claim 41 wherein the paternally imprinted QTL comprises at least a part of an insulin-like growth factor-2 gene (IGF-2).

45. (New) The method according to claim 41, wherein the paternally imprinted QTL comprises the insulin-like growth factor-2 (IGF-2) and a genetic marker characterized as nt241(G-A) or as Swc9.